AMENDMENT — VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification

Please amend the specification as follows:

On page 5, line 2, please delete "(SEQ ID NO: 3)" and insert--(SEQ ID NO: 1)--.

On page 5, line 4, please delete "(SEQ ID NO: 4)" and insert--(SEQ ID NO: 3)--.

On page 5, line 6, please delete "(SEQ ID NO: 12)" and insert--(SEQ ID NO: 11)--.

On page 5, line 13 please insert after the word MC4R--SEQ ID NO: 11--.

On page 5, line 14, please insert after P32245--(SEQ ID NO: 12)--.

On page 5, line 14, please insert after P70596--(SEQ ID NO: 13)--.

On page 5, line 14, please insert after P41983--(SEQ ID NO: 14)--.

On page 5, line 14, please insert after P56451--(SEQ ID NO: 15)--.

On page 5, line 15, please insert after P34974--(SEQ ID NO: 16)--.

On page 5, line 15, please insert after P41968--(SEQ ID NO: 17)--.

On page 5, line 15, please insert after P33033--(SEQ ID NO: 18)--.

On page 5, line 15, please insert after Q01718--(SEQ ID NO: 19)--.

On page 5, line 15, please insert after Q01726--(SEQ ID NO: 20)--.

On page 5, line 15, please insert after Q28031--(SEQ ID NO: 21)--.

On page 5, line 15, please insert after AF011466--(SEQ ID NO: 22)--.

On page 5, line 15, please insert after P21554--(SEQ ID NO: 23)--.

On page 5, line 15, please insert after P18089--(SEQ ID NO: 24)--.

On page 5, line 16, please insert after P30680--(SEQ ID NO: 25)--.

On page 5, line 16, please insert after P47211--(SEQ ID NO: 26)--.

On page 6, line 29, please delete "SEQ ID NO: 8" and insert--SEQ ID NO: 7--.

On page 6, line 29, please delete "SEQ ID NO: 9" and insert--SEQ ID NO: 8--.

On page 7, line 25, please delete "(SEQ ID NO: 6)" and insert--(SEQ ID NO: 5)--.

On page 7, line 26, please delete "(SEQ ID NO: 7)" and insert--(SEQ ID NO: 6)--.

On page 7, line 27, please delete "(SEQ ID NO: 8)" and insert--(SEQ ID NO: 7)--.

On page 7, line 28, please delete "(SEQ ID NO: 9)" and insert--(SEQ ID NO: 8)--.

On page 8, line 14, please delete "Taqman™" and insert--TAQMAN™--.

On page 10, line 5, please delete "(SEQ ID NO: 6)" and insert--(SEQ ID NO: 5)--.

On page 10, line 6, please delete "(SEQ ID NO: 7)" and insert—(SEQ ID NO: 6)--.

On page 11, line 28, please delete "(SEQ ID NOS: 2-5)" and insert--(SEQ ID NOS: 2-4)--.

On page 12, line 20, please delete "(SEQ ID NO: 8)" and insert--(SEQ ID NO: 7)--.

On page 12, line 21, please delete "(SEQ ID NO: 9)" and insert--(SEQ ID NO: 8)--.

On page 19, line 17, please delete "(SEQ ID NO: 6)" and insert--(SEQ ID NO: 5)--.

On page 19, line 18, please delete "(SEQ ID NO: 7)" and insert--(SEQ ID NO: 6)--.

On page 20, line 1, please delete "(SEQ ID NO: 10)" and insert--(SEQ ID NO: 9)--.

On page 20, line 2, please delete "(SEQ ID NO: 11)" and insert--(SEQ ID NO: 10)--.

In the Claims

Please amend the following claims:

1. (Twice Amended)

A method of identifying an animal which possesses a genotype [having a genetic marker] associated with variation in one or more favorable metabolic traits [such as] selected from fat content, growth rate, and feed consumption, the method comprising:

[a)] obtaining a nucleic acid sample from the animal; and

[b) identifying a genotype characterized by] assaying for the presence of a polymorphism in the [seventh transmembrane domain in the] MC4R [protein] gene [wherein, said genotype is] associated with variation in one or more of the metabolic traits [such as] of fat content, growth rate, and feed consumption.

2. (Twice Amended)

The method of claim 1 wherein the polymorphism is [characterized] identified [by a site specific mutation at amino acid position 298 in the seventh transmembrane domain of] at position 678 of a PCR sequence of the MC4R [protein] gene in pigs and [any] other animals.

4. (Twice Amended)

The method of claim 2 wherein the polymorphism [at amino acid position 298] is a guanine at base 678 in a PCR sequence of the MC4R gene associated with variation in fat content.

5. (Twice Amended)

The method of claim 2 wherein a marker for lower feed intake, than animals without the marker, is [identifiable] identified by [a mutation that replaces aspartic acid codon with asparagine codon at amino acid position 298] an adenine at base 678 of a PCR sequence of the MC4R [protein] gene.

6. (Twice Amended)

The method of claim 2 wherein a marker for faster rate of gain, than animals without the marker, is [identifiable] identified by [a mutation that replaces aspartic acid codon with asparagine codon at amino acid position 298 of] an adenine at base 678 of a PCR sequence of the MC4R [protein] gene.

10. (Twice Amended)

The method of claim 1 further comprising the step of amplifying polymorphism in the MC4R gene sequence with [allele specific oligonucleotide] primers.

20. (Twice Amended)

A method of identifying an animal which possess a desired genotype [having a genetic marker] associated with variation in one or more metabolic traits [such as] selected from fat content, growth rate, and feed consumption, the method comprising:

[a)] obtaining a nucleic acid sample from an animal;

[b)] amplifying nucleic acid of said sample with primers SEQ ID NO: 5 and SEQ ID NO: 6.

sequencing the amplified product to reveal a nucleotide substitution within a *Taq I* restriction enzyme recognition site;

[c)] digesting the [sample] amplified product with *Taq I* to obtain fragments;

[d)] separating the fragments obtained from the digestion, and

generating a MC4R gene fragment having one *Taq I* restriction site with primers SEQ ID NO: 9 and SEQ ID NO: 10; and

[e)] identifying the presence or absence of a *Taq I* site [in an MC4R gene fragment to specify polymorphic site]

wherein the presence of a *Taq I* restriction site identifies the presence of a polymorphic site in the MC4R gene associated with variation in one or more of the metabolic traits in the animal.

22. (Amended)

The method of claim 20 wherein the site is identifiable by fragments of 466, 225, and 76 bp when a guanine is present at base 678 of the amplified product and fragments of 542 and 225 bp when an adenine is present when a restriction enzyme which cuts at the same recognition site as *Taq I* is used.

23. (Twice Amended)

The method of claim 20 wherein the step of identifying comprises detecting [the] a *Taq I* restriction pattern.

28. (Twice Amended)

A method for selecting animals [for a] possessing a desired pair of alleles [desired polymorphic traits] associated with variation in one or more favorable metabolic traits selected from lower fat content, faster growth rate, or lower feed consumption, than animals without said [traits] alleles, comprising:

[a)] obtaining a nucleic acid sample from an animal;

[b) amplifying the nucleic acid of said sample];

[c)] identifying the alleles associated with a desired metabolic trait [a polymorphism characterized within a *Taq I* restriction recognition site], and

[d)] selecting the animals which have [a nucleotide substitution of guanine to adenine within the *Taq I* restriction site within the MC4R gene] desired alleles.

29. (Twice Amended)

A method for an indirect selection [for] of a polymorphism in a MC4R gene associated with variation in one or more metabolic traits selected from fat content, growth rate, and feed consumption comprising: [wherein specific alleles of an alternative DNA marker are used to make the indirect selection wherein the alternative DNA marker is a linked marker near MC4R comprising utilizing genetic linkage mapping techniques]

selecting specific alleles of an alternative DNA marker associated with the MC4R gene, wherein the MC4R gene is associated with a particular metabolic trait;

making an indirect selection of the polymorphism; and

establishing a linkage between the specific alleles of the alternative DNA and alleles of the DNA marker associated with the metabolic trait.

31. (Twice Amended)

A method of identifying animals[, which possesses a desired genotype having a genetic marker] to determine the association between a pair of alleles and one or more metabolic traits of interest [such as] selected from fat content, growth rate, and feed consumption [to determining the association between a MC4R genotype and a trait of interest], the method comprising:

[a)] obtaining a sample of animals from a line or breed of interest,

[b)] preparing genomic DNA from each animal in the sample,

[c)] determining the [genotype of the MC4R gene] alleles present, and

calculating the association between the [MC4R genotype] alleles and the trait.

32. (Twice Amended)

A method of selecting animals which possess a desired MC4R genotype [having a genetic marker] associated with variation in one or more metabolic traits [such as] selected from fat content, growth rate, and feed consumption, the method comprising:

[a)] obtaining a nucleic acid sample from an animal;

[b)] identifying the genotype of the MC4R gene of the animal; and

[c)] selecting those animals which have the genotype associated with the desired traits.

33. (Amended)

A method of identifying an animal which possesses a desired polymorphism within the melanocortin-4 receptor protein of the seventh transmembrane domain at amino acid 298 comprising:

[a] obtaining a nucleic acid sample from an animal; and

[b)] identifying the polymorphism in the translated [by a nucleotide substitution within a *Taq I* site specific restriction pattern of the] MC4R gene

wherein an aspartic acid at amino acid 298 identifies leanness and lower feed intake, than animals without the polymorphism and an asparagine at amino acid 298 identifies a faster rate of gain than animals without the polymorphism.